

Exhibit B

>AF059485 ACCESSION:AF059485 NID: gi 3170614 gb AF059485.1 AF059485
Mus musculus DOC4 (Doc4) mRNA, complete cds
Length = 9722

Score = 5272 bits (13524), Expect = 0.0
Identities = 2498/2591 (96%), Positives = 2542/2591 (97%), Gaps = 2/2591 (0%)
Frame = +1

Query: 165 DHPGGLQNHARLRTPPPPPLSHAHTPNQHHAASINSLNRGNFTPRSNPSPAPTDHSLSGEP 224
DHP LQNH RLRTPPPPPL HAHTPNQHHAASINSLNRGNFTPRSNPSPAPTDHSLSGEP
Sbjct: 1285 DHPSSLQNHPRRLRTPPPPPLPHAHTPNQHHAASINSLNRGNFTPRSNPSPAPTDHSLSGEP 1464

Query: 225 PAGGAQEPAPAHAQENWLLNSNIPLSTRNLGKQPFLGTLQDNLIEMDILGASRHDGAYSDDGH 284
PAG AQEP HAQ+NW+LNS IP+ETRNLGKQPFLGT QDNLIEMDI ASR DGAYSDDGH
Sbjct: 1465 PAGSAQEPHTAQDNWVLNSKIPVETRNLGKQPFLGTWQDNLIEMDIFASRRDGAYSDDGH 1644

Query: 285 FLFKPGGTSPLFCTTSPGYPLTSSTVYSPPPRPLPRSTFARPAFNLKKPSKYCNWKCAAL 344
F FKPGGTSPLFCTTSPGYPLTSSTVYSPPPRPLPRSTF+RPAFNLKKPSKYCNWKCAAL
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Query: 345 SAIVISATLVILLAYFVAMHLFGLNWHLQPMEGQM--YEITEDTASSWPVPTDVSILYPSG 402
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Query: 403 GTGLETDPDRKGKGTTEGKPSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIDHPV 462
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Sbjct: 2185 HLKFNVSILGKAALVGIYGRKGLPPSHTQLDFVELLDGRRLLTQEARSLGEPQRQSRGPVP 2364

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HGTFLPDTGLC+CDPSWTGHDCSIEICAADCGGHGVCVGGTCRCEDGWMGAACDQRACHP
Sbjct: 2905 HGTFLPDTGLCNCDPSWTGHDCSIEICAADCGGHGVCVGGTCRCEDGWMGAACDQRACHP 3084

Query: 763 RCAEHGTCRDGKCECSPGWNGEHCTIEGCPGLCNGNGRCTLDLNGWHVCQLGWRGAGCD 822
RCAEHGTCRDGKCEC+PGWNGEHCTIEGCPGLCNGNGRCTLDLNGWHVCQLGWRG GCD
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TSMET CGD KDNDDGDLVDCMDPDCCLQPLCH+NPLCLGSP+PLDIIQETQ VPSQQNL
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DLSNFARPNPVVSPSPLTSFASSCAEKGPVPEIQALQEEI I+GCKMRLSYLSSRTPGY
Sbjct: 3805 DLSNFARPNPVVSPSPLTSFASSCAEKGPVPEIQALQEEIVIAGCKMRLSYLSSRTPGY 3984

Query: 1063 KSVLRISLTHPTIPFNLMKVHLMVAVEGRLFRKWFAAAPDLSYYFIWDKTDVYNQKVFGL 1122
KSV+RISLTHPTIPFNLMKVHLMVAVEGRLFRKWFAAAPDLSYYFIWDKTDVYNQKVFGL
Sbjct: 3985 KSVVRISLTHPTIPFNLMKVHLMVAVEGRLFRKWFAAAPDLSYYFIWDKTDVYNQKVFGL 4164

Query: 1123 SEAFVSVGYEYESCPDLILWEKRTTVLQGYEIDASKLGGWSLDKHHALNIQSGILHKGN 1182
SEAFVSVGYEYESCPDLILWEKRT VLQGYEIDASKLGGWSLDKHHALNIQSGILHKGN
Sbjct: 4165 SEAFVSVGYEYESCPDLILWEKRTAVLQGYEIDASKLGGWSLDKHHALNIQSGILHKGN 4344

Query: 1183 ENQFVSQQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYI 1242
ENQFVSQQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYI
Sbjct: 4345 ENQFVSQQPPVIGSIMGNRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYI 4524

Query: 1243 RRIFPSGNVTNILELSHSPAHHKYLLATDPMMSGAVFLSDSNSRRVFKIKSTVVVKDLVKNS 1302
RRIFPSGNVTNILE+SHSPAHHKYLLATDPMMSGAVFLSD+NSRRVFK+KST VVKDLVKNS
Sbjct: 4525 RRIFPSGNVTNILEMSHSPAHHKYLLATDPMMSGAVFLSDTNSRRVFKVKSTTVVKDLVKNS 4704

Query: 1303 EVVAGTGDQCLPFDDTRCGDGGKATEATLTNPRGITVDKFGLIYFVDGTMIRRIDQNGII 1362
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STLLGSNDLTSARPLSCDSVM+ISQV LEWPTDLAINPMDNSLYVLDNNVVLQISENHQV
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Query: 1423 RIVAGRPMHCQVPGIDHFLLSKVAIHATLESATALAVSHNGVLYIAETDEKKINRIRQVT 1482
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 Sbjct: 6145 NVTLPIDNGLNLVEWRQRKEQARGQVTVFGPRLRVHNRNLLSLDFDRVTRTEKIYDDHRK 6324

Query: 1843 FTLRILYDQAGRPSLWSPSSRLNGVNVITYSPGGYIAGIQRGIMSERMEYDQAGRITSRIF 1902
 FTLRILYDQAGRPS WSPSSRLNGVNVITYSPGG+IAGIQRGIMSERMEYDQAGRITSRIF
 Sbjct: 6325 FTLRILYDQAGRPSFWSPPSSRLNGVNVITYSPGGHIAGIQRGIMSERMEYDQAGRITSRIF 6504

Query: 1903 ADGKTWSYTYLEKSMVLLHLSQRQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNI 1962
 ADGK WSYTYLEKSMVL LHSQRQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNI
 Sbjct: 6505 ADGKMWSYTYLEKSMVLLHLSQRQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNI 6684

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 YQPPEGNASVIQDFTEDGHLHLYFYLTGRRVIYKYGKLSKLAETLYDTTKVSFTYDETA
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misc_feature

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/note="putative; transmembrane-region site"

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